

73086  
JCL

**From:** Fredman, Jeffrey  
**Sent:** Monday, August 12, 2002 2:31 PM  
**To:** STIC-Biotech/ChemLib  
**Cc:** Angell, Jon E  
**Subject:** FW: Sequence Database Search Request

PLEASE RUSH.

I APPROVE.

Jeff Fredman  
(Eric, I got it the second after I called you)

-----Original Message-----

**From:** Angell, Jon E  
**Sent:** Monday, August 12, 2002 2:31 PM  
**T :** Fredman, Jeffrey  
**Subject:** Sequence Database Search Request

**Point of Contact:**  
Mona Smith  
Technical Information Specialist  
CM1 6A01  
Tel: 308-3278

### SEARCH REQUEST FORM

Scientific and Technical Information Center

Examiner# : 78697  
Art Unit : 1635  
Phone Number: 605-1165  
Date: 8/12/02  
Serial Number: 09/786,043  
Mailbox & Bldg/Room Location: CM1-11E12  
Results Format Preferred (circle): Paper

I would like to have a search performed using the following SEQ. ID NOs. from application : 09/786,043

SEQ ID NO. 1-- nucleic acid seq. (<900nucleotides in length)  
SEQ ID NO. 2-- amino acid seq. (255 amino acids in length)

NOTE: Please reverse transcribe SEQ ID NO:2 into nucleic acid encoding the seq of SEQ ID NO:2.

I would like a standard search of SEQ ID NO.1 and the cDNA encoding SEQ ID NO:2 , AND an oligomer search of the cDNA encoding SEQ ID NO:2 to identify nucleotide oligos encoding at least 10 contiguous amino acids of SEQ ID NO: 2.

Thanks,  
Eric

*J. Eric Angell*  
Art Unit 1635  
CM1 12D15  
703-605-1165  
mailbox CM1 11E12

Searcher: M. Smith  
Phone: \_\_\_\_\_  
Location: \_\_\_\_\_  
Date Picked Up: 8/15/02  
Date Completed: 8/14/02  
Searcher Prep/Review: 10  
Clerical: \_\_\_\_\_  
Online time: 15

TYPE OF SEARCH:  
NA Sequences: 1  
AA Sequences: 3  
Structures: \_\_\_\_\_  
Bibliographic: \_\_\_\_\_  
Litigation: \_\_\_\_\_  
Full text: \_\_\_\_\_  
Patent Family: \_\_\_\_\_  
Other: \_\_\_\_\_

VENDOR/COST (where applic.)  
STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
Questel/Orbit: \_\_\_\_\_  
DRLink: \_\_\_\_\_  
Lexis/Nexis: \_\_\_\_\_  
Sequence Sys.: \_\_\_\_\_  
WWW/Internet: \_\_\_\_\_  
Other (specify): \_\_\_\_\_

RECEIVED  
JULY 12 2002  
TECHNICAL INFORMATION CENTER

|   |   |
|---|---|
| DR  | InterPro: IPR003118; SAM_PNT.   |
| DR  | Pfam: PF00178; Ets: 1.  |
| DR  | PRINTS: PR00454; ETS_DOMAIN.  |
| DR  | SMART: SM00413; ETS_PNT: 1.   |
| DR  | PROSITE: PS50061; ETS_DOMAIN_3: 1.  |
| SO  | SEQUENCE 300 AA; 34893 MW; 51CB6E6195E4E06 CRC64;   |
| Query Match   | Best Local Similarity 40.7%; Score 574; DB 4; Length 300; Matches 117; Conservative 41.3%; Pred. No. 2. 6e-47; Mismatches 63%; Indels 56; Gaps 8; |
| Oy  | 22 SWTDLFSNEEYYPAPNQHOTACDSWYTSHPEYWTKRHWEMLQFCDCDQYKLDNCIFRCN 81   |
| Db  | 23 AWTDSPYCPCNVSSGF---FGSQWHEIHPQWTKYQWEMLOHLIDTNOLDASCIPQE 77  |
| Oy  | 82 FNISGLQCSMTOEEFYEAAGCCEGYLYFILONIRTQG-----YSFENDAEESKA 131   |
| Db  | 78 FDISGERLCSMSLQEFTRAAGSAGQLYLSNQHLKINGQCCSDLFQSAHNIVKTQDP 137   |
| Oy  | 132 TIKD-YADSNCL-----KTSGI-----KSQD---C 152   |
| Db  | 138 SIMTWKEWNLIDTNYGSTVDLDSKFCRQISMUTISHPVAESPDMKKQDPPAEC 197   |
| Oy  | 153 PSSRTSPOSSHWEFRDLILSPEENCGILEWEDREGIFRVKSALAKWNGORKND 212   |
| Db  | 198 HT-KKHNPRGTHLWEFIRDILNLPDKNPGLIKEDSEGVRFLKSEAVADGKKNNS 256  |
| Oy  | 213 RMTYEKLRSRALRYYYKIGLERD-RRLVVKFGKNAHGQEDK 254   |
| Db  | 257 SMTYEKLRSRAMYYKREIELERVGDGRLLVKFGKNAHGRENE 299  |
| RESULT 12   | 070273  |
| ID  | 070273  |
| AC  | 070273;   |
| DT  | 01-AUG-1998 (TREMBlre. 07, Created)   |
| DT  | 01-DEC-2001 (TREMBlre. 07, Last sequence update)  |
| DE  | EHF.  |
| GN  | MUS   |
| OS  | Mus musculus (Mouse).   |
| OC  | OC  |
| OX  | OX  |
| SEQUENCE FROM N.A.  | NCBI_TaxId=10090;   |
| NC  | RN [1]-   |
| RX  | RP  |
| RA  | RA  |
| RT  | RA  |
| "Borchert M.A., Kleinbaum L.A., Sun L.Y., Burton F.H.; Molecular cloning and expression of Ehf, a new member of the ets transcription factor/oncoprotein gene family."; | Strausberg R.; Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.  |
| RL  | EMBL: BC005520; AJ005520.1; -   |
| Biochem. Biophys. Res. Commun. 246:176-181(1998).   | DR HSSP; Q00422; IAWC.  |
| DR  | InterPro: IPR00418; Ets.  |
| DR  | InterPro: IPR002341; HSF_ETS.   |
| DR  | InterPro: IPR003118; SAM_PNT.   |
| DR  | Pfam: PF00178; Ets: 1.  |
| DR  | PRINTS: PR00454; ETS_DOMAIN.  |
| DR  | PROSITE: PS50061; ETS_DOMAIN_3: 1.  |
| SO  | SEQUENCE 285 AA; 33225 MW; 9138C527C65955F CRC64;   |
| Query Match   | Best Local Similarity 36.5%; Score 514; DB 11; Length 285; Matches 112; Conservative 39.7%; Pred. No. 3e-41; Mismatches 64; Indels 69; Gaps 8;    |
| Oy  | 22 SWTDLFSNEEYYPAPNQHOTACDSWYTSHPEYWTKRHWEMLQFCDCDQYKLDNCIFRCN 81   |
| Db  | 23 AWTDSPYCPCNVSSGF---FGSQWHEIHPQWTKYQWEMLOHLIDTNOLDASCIPQE 75  |
| Oy  | 82 FNISGLQCSMTOEEFYEAAGCCEGYLYFILONIRTQG-----YSFENDAEESKA 130   |
| Db  | 76 SIMTWKEWNLIDTNYGSTVDLDSKFCRQISMUTISHPVAESPDMKKQDHPVKS 120  |
| Oy  | 121 SFENDAE-----SKATIKD-YADSNCLKTSGI-----KSQD---CHS 154   |
| Db  | 123 SIMTWKEWNLIDTNYGSTVDLDSKFCRQISMUTISHPVAESPDMKKQDHPVKS 155 HSR-TSLOSSHWEFRDLILSPEENCGILEWEDREGIFRVVSALAKWNGORKND 213                           |
| Oy  | 183 HTKHNPRGTHLWEFIRDILNLPDKNPGLIKEDSEGVRFLKSEAVOLWGGKKNNSS 242   |
| Query Match   | Similarity 40.3%; Score 568; DB 11; Length 300; Pred. No. 9. 9e-47;   |

Aug 27, 1998

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: August 13, 2002, 21:21:50 ; Search time 88.19 Seconds

(without alignments)  
500.212 Million cell updates/sec

Title: US-09-786-043-2

Perfect score: 1409

Sequence: 1 MLDSVTHSTFLPNASFCDFPL.....DRRLVYKFGKNAHGHQEDKL 255

Scoring table: BLOSUM62

GapOp 10.0 , Gapext 0.5

Searched: 5622222 seqs, 17294929 residues

total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Maximum Match 0\*

Listing first 45 summaries

Database : SPTRIMBL\_19;\*

1: sp\_archaea;\*

2: sp\_bacteria;\*

3: sp\_fungi;\*

4: sp\_human;\*

5: sp\_invertebrate;\*

6: sp\_mammal;\*

7: sp\_mhc;\*

8: sp\_organelle;\*

9: sp\_phage;\*

10: sp\_plant;\*

11: sp\_rabbit;\*

12: sp\_virus;\*

13: sp\_vertebrate;\*

14: sp\_unclassified;\*

15: sp\_virus;\*

16: sp\_bacteriap;\*

17: sp\_archeap;\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query | Match | Length | DB ID  | Description        |
|------------|-------|-------|-------|--------|--------|--------------------|
| 1          | 1409  | 100.0 | 255   | 4      | 095175 | 095175 homo sapien |
| 2          | 1409  | 100.0 | 265   | 4      | 0950Y3 | Q9qy3 homo sapien  |
| 3          | 1406  | 99.8  | 255   | 4      | 09URW5 | Q9ukw5 homo sapien |
| 4          | 1406  | 99.8  | 265   | 4      | 09URW6 | Q9ukw6 homo sapien |
| 5          | 1338  | 95.0  | 253   | 11     | 0921H5 | Q921H5 mus musculu |
| 6          | 1330  | 94.4  | 253   | 11     | 0922K6 | Q922K6 mus musculu |
| 7          | 588.5 | 41.8  | 277   | 4      | 095Y5  | Q95Y5 homo sapien  |
| 8          | 584.5 | 41.5  | 277   | 4      | 09H509 | Q9H509 homo sapien |
| 9          | 578   | 41.0  | 300   | 4      | Q95V4  | Q95V4 homo sapien  |
| 10         | 574   | 40.7  | 300   | 4      | Q9ZC4  | Q9ZC4 homo sapien  |
| 11         | 574   | 40.7  | 300   | 4      | Q9KF9  | Q9KF9 homo sapien  |
| 12         | 568   | 40.3  | 300   | 11     | 09273  | 09273 mus musculu  |
| 13         | 514.5 | 36.5  | 285   | 11     | 099K12 | Q99K12 mus musculu |
| 14         | 430.5 | 30.6  | 371   | 11     | 05275  | 05275 mus musculu  |
| 15         | 427.5 | 30.3  | 348   | 4      | Q9918  | Q9918 homo sapien  |
| 16         | 422   | 30.0  | 371   | 4      | P78545 | P78545 homo sapien |

Query Match 100.0%; Score 1409; DB 4; Length 255;  
Best Local Similarity 100.0%; Pred. No. 6.1e-128; Mismatches 0; Indels 0; Gaps 0;

[1] SEQUENCE FROM N.A. MEDLINE=99054671; PubMed=9840936;  
RX Zhou J., Ng A.Y., Tymms M.J., Jermini L.S., Seth A.K., Thomas R.S., RA Kola I.; RT "A novel transcription factor, ELF5, belongs to the ELF subfamily of ETS genes and maps to human chromosome 11p13-15, a region subject to LOH and rearrangement in human carcinoma cell lines." RL Oncogene 17:2719-2732(1998). DR AF049703; AAC79755.1; DR HSSP; Q00422; 1AWC. DR InterPro; IPR000418; Ets. DR InterPro; IPR00241; HSF\_ETS. DR InterPro; IPR003118; SAM\_PNT. DR Pfam; PF00178; Ets; 1. DR Pfam; PF02198; SAM\_PNT; 1. DR PRINTS; PRO0454; ETSDOMAIN. DR SMART; SM00413; Ets; 1.. DR SMART; SM00251; SAM\_PNT; 1. DR PROSITE; PSS0061; ETS\_DOMAIN; 1. SQ SEQUENCE 255 AA; 30121 MW; AE61C5B178ECB555 CRC64;



|    |   |                       |   |
|----|---|-----------------------|---|
| RA | Akbarali Y., Finger E., Boltax J., Endress G., Munger K., Kunsch C., Libermann T.A.; "Characterization of ESE-2, a novel ESE-1-related Ets transcription factor that is restricted to glandular epithelium and differentiated keratinocytes."; J. Biol. Chem. 274:29439-29452 (1999). | Qy                    | 61 EWLOFCCDQYKLDTNCISFCNPNSGLQCSMTOEFEVAAAGCGRYLYFILQNIRTOGY 120  |
| RT |   | Db                    | 61 EWLOFCCDQYKLDTNCISFCNPNSGLQCSMTOEFEVAAAGCGRYLYFILQNIRTOGY 120  |
| RT |   | Qy                    | 121 SFENDAESKATIKDYADSNCNLKTSGIKSQQDCHSHSRSTSLOSSHLWEFVDRLLSPEENC 180   |
| RT |   | Db                    | 121 SFENDAESKATIKDYADSNCNLKTSGIKSQQDCHSHSRSTSLOSSHLWEFVDRLLSPEENC 180   |
| RL | EMBL; AP1540.; ADD2960.1; -.  | Qy                    | 181 GILEWEDREQIFRVKSEALAKMGRKRNDRMTYEKLSSRALYYTKTGILERVDRRLV 240  |
| DR | InterPro; IPRO000418; ETS.  | Db                    | 179 GILEWEDREQIFRVKSEALAKMGRKRNDRMTYEKLSSRALYYTKTGILERVDRRLV 238  |
| DR | InterPro; IPRO02341; HSF-ETS.   | Qy                    | 241 YKEFGNAHGWQEDKL 255   |
| DR | InterPro; IPRO003118; SAM_PNT.  | Db                    | 239 YKEFGNAHGWQEEKL 253   |
| DR | Pfam; PF00178; ETS; 1.  |                       |   |
| DR | Pfam; PF0198; SAM_PNT; 1.   |                       |   |
| DR | PRINTS; PR00054; ETS DOMAIN.  |                       |   |
| DR | SMART; SM00413; ETS; 1.   |                       |   |
| DR | SMART; SM00251; SAM_PNT; 1.   |                       |   |
| DR | PROSITE; PS50061; ETS DOMAIN 3; 1.  |                       |   |
| SQ | SEQUENCE . 265 AA; 31295 MW; B2921A79A45768E3 CRC64;  | RESULT                | 6   |
|    |   | 0922K6                | PRELIMINARY;  |
|    |   | ID                    | PRT; 253 AA.  |
|    |   | AC                    |   |
|    |   | DT                    | 01-MAY-1999 (TREMBLrel. 10, Created)  |
|    |   | DT                    | 01-MAY-1999 (TREMBLrel. 10, Last sequence update)   |
|    |   | DT                    | 01-DEC-2001 (TREMBLrel. 19, Last annotation update)   |
|    |   | DE                    | E74-LIKE FACTOR 5.  |
|    |   | GN                    | ELF5.   |
|    |   | OS                    | Mus musculus (Mouse).   |
|    |   | OC                    | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  |
|    |   | OX                    |   |
|    |   | RN                    | [1]   |
|    |   | RP                    | SEQUENCE FROM N.A.  |
|    |   | RX                    | LINE-99054671; PubMed=9840936;  |
|    |   | RA                    | Zhou J., Ng A.Y., Tytms M.J., Jermyn L.S., Seth A.K., Thomas R.S., Kola I.; "A novel transcription factor, ELF5, belongs to the ELF subfamily of RT genes and maps to human chromosome 11p13-15, a region subject to LOH and rearrangement in human carcinoma cell lines."; Oncogene 17:2711-2732 (1998). |
|    |   | RA                    | DR  |
|    |   | RA                    | HSSP; Q00422; IANC.   |
|    |   | DR                    | MGI; 1335079; Elif5.  |
|    |   | DR                    | InterPro; IPR000418; Ets.   |
|    |   | DR                    | InterPro; IPR02341; HSF_ETS.  |
|    |   | DR                    | InterPro; IPR003118; SAM_PNT.   |
|    |   | DR                    | PFAM; PF00178; Ets.   |
|    |   | DR                    | Pfam; PF02198; SAM_PNT; 1.  |
|    |   | DR                    | PRINTS; PR00054; ETS DOMAIN.  |
|    |   | DR                    | SMART; SM00413; ETS; 1.   |
|    |   | DR                    | SMART; SM0051; SAM_PNT; 1.  |
|    |   | DR                    | PROSITE; PS50061; ETS DOMAIN 3; 1.  |
|    |   | SQ                    | SEQUENCE . 253 AA; 29971 MW; 3FD028DA77AFCE48 CRC64;  |
|    |   | RESULT                | 5   |
|    |   | 0921HS                | PRELIMINARY;  |
|    |   | AC                    | PRT; 253 AA.  |
|    |   | DT                    |   |
|    |   | DT                    | 01-DEC-2001 (TREMBLrel. 19, Created)  |
|    |   | DT                    | 01-DEC-2001 (TREMBLrel. 10, Last sequence update)   |
|    |   | DT                    | 01-DEC-2001 (TREMBLrel. 19, Last annotation update)   |
|    |   | DE                    | SIMILAR TO E74-LIKE FACTOR 5.   |
|    |   | OS                    | Mus musculus (Mouse).   |
|    |   | OC                    | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  |
|    |   | OX                    |   |
|    |   | RN                    | [1]   |
|    |   | RP                    | SEQUENCE FROM N.A.  |
|    |   | RA                    | Strassberg R.; Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.  |
|    |   | DR                    | EMBL; BC012424; AAH12424.1; -.  |
|    |   | SQ                    | SEQUENCE . 253 AA; 29872 MW; 3FC4799F77AFCF48 CRC64;  |
|    |   | Query Match           | 94.4%; Score 1330; DB 11; Length 253;   |
|    |   | Best Local Similarity | 94.4%; Prod. No. 2.5e-120;  |
|    |   | Matches 240;          | Conservative 8; Mismatches 5; Indels 2; Gaps 1;   |
|    |   | Qy                    | 1 MLD5VTHSTFLPNASCDPLMSWTDLSNEEYYPAFEHQTACDSYNTSVHPEYWTKRHW 60  |
|    |   | Db                    | 1 MLD5VTHSTFLPNASCDPLMSWTDLSNEEYYPAFEHQTACDSYNTSVHPEYWTKRHW 60  |
|    |   | Query Match           | 95.0%; Score 1338; DB 11; Length 253;   |
|    |   | Best Local Similarity | 94.5%; Prod. No. 4.2e-121;  |
|    |   | Matches 241;          | Conservative 8; Mismatches 14; Indels 2; Gaps 1;  |
|    |   | Qy                    | 1 MLDSVTHSTFLPNASCDPLMSWTDLSNEEYYPAFEHQTACDSYNTSVHPEYWTKRHW 60  |
|    |   | Db                    | 1 MLDSVTHSTFLPNASCDPLMSWTDLSNEEYYPAFEHQTACDSYNTSVHPEYWTKRHW 60  |



|  |   |
|--|---|
| RT ESE-1."   | SEQUENCE FROM N.A.  |
| RL J. Biol. Chem. 275:2986-2998(2000).                                 | RA Mitchell S.C., Levin E., Hubert R., Yeramian C., Saffran D.C., Afar D.E.H.; RT "Up-Regulation of the Epithelial-Specific Transcription Factor Genes hESF and ESX in Advanced prostate Cancer." |
| DR EMBL; AF24439; IPR00418; Ets.                                       | RT Prostate 0:0-0.1999.   |
| DR HSSP; Q00422; IAWC.   | DR AF212848; AA61670; 1;  |
| DR InterPro; IPR002341; HSF_ETS.                                       | DR ALI5752; CAC1701; 1;   |
| DR InterPro; IPR00116; SAM_PNT.  | DR AF03977; AAC35644; 1;  |
| DR Pfam; PF00198; Ets; 1.  | DR HSSP; 000422; IAWC.  |
| DR PRINTS; PRO0154; ETS_DOMAIN.  | DR InterPro; IPR00416; Ets.   |
| DR SMART; SM00413; Ets; 1.   | DR InterPro; IPR00231; HSF_ETS.   |
| DR SMART; SM00251; SAM_PNT; 1.   | DR InterPro; IPR003118; SAM_PNT.  |
| DR PROSITE; PS50061; ETS_DOMAIN_3; 1.                                  | DR Pfam; PF00178; Ets; 1.   |
| SEQUENCE 300 AA; 34920 MW;   | DR PRINTS; PRO0422; ETS_DOMAIN; 1.  |
| DR PRINTS; PRO0422; IAWC.  | DR SMART; SM00413; Ets; 1.  |
| DR SMART; SM00251; SAM_PNT; 1.   | DR PROSITE; PS50061; ETS_DOMAIN_3; 1.   |
| DR PROSITE; PS50061; ETS_DOMAIN.                                       | SEQUENCE 300 AA; 34892 MW; 5ACBB38BAF852ED0 CRC64;  |
| Query Match 41.0%; Score 578; DB 4; Length 300;                        | Query Match 40.7%; Score 574; DB 4; Length 300;   |
| Best Local Similarity 41.7%; Pred. No. 1.1e-47;                        | Best Local Similarity 41.3%; Pred. No. 2.6e-47;   |
| Matches 118; Conservative 47; Mismatches 62;                           | Matches 117; Conservative 47; Mismatches 63;  |
| Indels 56; Gaps 8;   | Indels 56; Gaps 8;  |
| Db 22 SMTDLSNEEYYPAFEHOTACDSYWTWSHPEWTKRHYWEWLQFCDCOYKLDTNICISFCN 81   | Db 22 SMTDLSNEEYYPAFEHOTACDSYWTWSHPEWTKRHYWEWLQFCDCOYKLDTNICISFCN 81  |
| Db 23 AWTDYSPTCNVSSGF -----FGSQWHEIHPQWTKYQOWENLQLHDTNOLDANCIPFQE 77   | Db 23 AWTDYSPTCNVSSGF -----FGSQWHEIHPQWTKYQOWENLQLHDTNOLDANCIPFQE 77  |
| Qy 82 FNTSGLQLCSMTQEFYEAAGLGEYLFLONIRTG -----YSFFNDAAEBSKA 131         | Qy 82 FNTSGLQLCSMTQEFYEAAGLGEYLFLONIRTG -----YSFFNDAAEBSKA 131  |
| Db 78 FDINGEHCMSLMSQETRAAGTAGQOLLYSNLQHLWNGQCSSLDFQSTHNVTKTEQTEP 137   | Db 78 FDINGEHCMSLMSQETRAAGTAGQOLLYSNLQHLWNGQCSSLDFQSTHNVTKTEQTEP 137  |
| Qy 132 TIKD-YADSNCI-----KTSGI-----RSQD----C 152                        | Qy 132 TIKD-YADSNCI-----KTSGI-----RSQD----C 152   |
| Db 138 SIMNTWDENLYDNTNNGSTVLLDGKTFCRVQISMTTSHPVAEASPDMKKEQDPACK 197    | Db 138 SIMNTWDENLYDNTNNGSTVLLDGKTFCRVQISMTTSHPVAEASPDMKKEQDPACK 197   |
| Qy 153 HSHSRSTSLOSSHLWEFYRDLLSPENCNGILEMEDREQIFRVVKSEALAKWQQRKKND 212  | Qy 153 HSHSRSTSLOSSHLWEFYRDLLSPENCNGILEMEDREQIFRVVKSEALAKWQQRKKND 212   |
| Db 198 HF-KHAPRGTHLWEFTDILLNPDKNGPLKTFWDRSEGVRFLKSEAVAQLWGGKKNN 256    | Db 198 HF-KHAPRGTHLWEFTDILLNPDKNGPLKTFWDRSEGVRFLKSEAVAQLWGGKKNN 256   |
| Qy 213 RMYTEKLSRALRYYYKGILERD-RFLVYKEGKGNAHGQWEKD 254                  | Qy 213 RMYTEKLSRALRYYYKGILERD-RFLVYKEGKGNAHGQWEKD 254   |
| Db 257 SMTYEKLSRAMYYKKREILLEVDGRLVYKEGKGNAHGWRNE 299                   | Db 257 SMTYEKLSRAMYYKKREILLEVDGRLVYKEGKGNAHGWRNE 299  |
| RESULT 10  | RESULT 11   |
| Q9NZC4 PRELIMINARY; PRT; 300 AA.                                       | Q9UKF9 PRELIMINARY; PRT; 300 AA.  |
| AC Q9NZC4  | ID Q9UKF9   |
| DT 01-OCT-2000 (TREMBLrel. 15, Created)                                | AC Q9UKF9   |
| DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)                   | DT 01-MAY-2000 (TREMBLrel. 13, Created)   |
| DE ETS DOMAIN TRANSCRIPTION FACTOR (DJ8/5K15.1.2).                     | DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  |
| GN Homo sapiens (Human)  | DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  |
| OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;   | DE ETS_HOMOLOGOUS_FACTOR.   |
| RA Brooks-Wilson A.R.; Miller A., North M.; McCormick M.K.;            | GN Homo sapiens (Human)   |
| RA Mushegian A.; Carlee L.; Watanskul T.; Chu S.; Emtage S.,           | OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  |
| RA McCormick M.K.;   | RN [1] SEQUENCE FROM N.A.   |
| RN [1]   | OX NCBI_TAXID=9606;   |
| RP SEQUENCE FROM N.A.  | OX NCBI_TAXID=9606;   |
| RA Tugores A.; Le J.; Sorokina I.; Sniders A.J.; Duyao M.; Reddy P.S., | RN [1] SEQUENCE FROM N.A.   |
| RA Mushegian A.; Carlee L.; Watanskul T.; Chu S.; Emtage S.,           | RP TISSUE=PROSTATE;   |
| RA McCormick M.K.;   | RX MEDLINE=99c58631; PubMed=10527851;   |
| RP SEQUENCE FROM N.A.  | RA Kleinbaum L.A., Duggan C., Ferreira E., Coffey G.P., Buttice G., Burton F.H.;  |
| RA Tugores A.; Le J.; Sorokina I.; Sniders A.J.; Duyao M.; Reddy P.S., | RT "Human chromosomal localization, tissue/tumor expression, and regulatory function of the ets family gene EHF";   |
| RA Mushegian A.; Carlee L.; Watanskul T.; Chu S.; Emtage S.,           | RL Biochim. Biophys. Commun. 264:119-126 (1999).  |
| RA McCormick M.K.;   | DR EMBL; AF170583; AAC05998; 1;   |
| RT A Novel Epithelial Specific ETS Transcription Factor, ESEJ, is a    | DR HSSP; Q00422; IAWC.  |
| RT Negative Modulator of MAP Kinase Signaling Pathways, and its        | DR InterPro; IPR000418; Ets.  |
| RT Expression is Lost in Carcinomas."                                  | DR InterPro; IPR002341; HSF_ETS.  |
| RT Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.            | DR InterPro; IPR002341; HSF_ETS.  |
| RT Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.            | DR InterPro; IPR002341; HSF_ETS.  |
| RA Hall R.;  | DR InterPro; IPR000418; Ets.  |
| RA Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.            | DR InterPro; IPR002341; HSF_ETS.  |
| RN [4]   | DR InterPro; IPR002341; HSF_ETS.  |

|                       |  |                       |  |   |  |   |  |                       |  |                       |  |
|-----------------------|--|-----------------------|--|---|--|---|--|-----------------------|--|-----------------------|--|
| DR                    | InterPro; IPR003118; SAM_PNT.  | Matches               | 120;   | Conservative  | 39;  | Mismatches  | 69;  | Indels                | 54;  | Gaps                  | 7;   |
| Pfam                  | PF00178; Ets_1.  | Qy                    | 22   | SWTDLFSNEEYPAFEHQTCDSYWTSHVPEYTKHVNWELQFCDCQYKLDTCISFCN 81    | DR   | 23  | AWTDSYPTCNVSSGF-----FGSQWHEIHPQYWTKYQWENLQHILDTNOLDASCIPFQE 77   |                       |  |                       |  |
| DR                    | PFO0198; SAM_PNT; 1.   | Db                    | 82   | FNISGLQCSMTQEFVEAGLCGEYLFLQNIERTGY-----                       | DR   | 82  | FNISGLQCSMTQEFVEAGLCGEYLFLQNIERTGY-----  |                       |  |                       |  |
| DR                    | SMART; SN00413; Ets_1.   | Qy                    | 121  | SFFNDAEE-----SKATIKDADSNCLKTSGI-----KSQD--CHS 154             | DR   | 78  | FDISGEHLCSMSLQEFTRAGSAGQLYSNLQHJKWNGCSSLDFQSAHNIVKTVTEQTDP 137   |                       |  |                       |  |
| DR                    | SMART; SN00251; SAM_PNT; 1.  | Db                    | 128  | SIANTWKEENLYDPSSYGTVDLDSKTCRAQISMSTSMLPVAESPDMKKEODHPVKRS 197 | DR   | 155   | HSRT-SLOSSHLWEFVRDILLSPENCGILEWEDEREGIIFRVVKSEALAKMKGORKKNDR 213   |                       |  |                       |  |
| PROSITE               | PS50061; ETS_DOMAIN_3; 1.  | Qy                    | 121  | SFFNDAEE-----SKATIKDADSNCLKTSGI-----KSQD--CHS 154             | Db   | 198   | HTKKHNPRTGTHWEIFRDILLSPDKNPGLIKEDRSEGVTFLKSEAVQLWGKKNNSS 257   |                       |  |                       |  |
| SEQUENCE              | 300 AA; 34893 MN; 5ICB68BE195EA06 CRC64;   | Db                    | 138  | SIANTWKEENLYDPSSYGTVDLDSKTCRAQISMSTSMLPVAESPDMKKEODHPVKRS 197 | DR   | 214   | MTYEKLSSRLRYYYKTGILERVDRRLVYKFGNAHGWQDK 254  |                       |  |                       |  |
| DR                    | 78 FDINGEHLCSMSLQEFTRAGTAGQLYSLQHJKWNGCSSLDFQSAHNIVKTVTEQTDP 137   | Qy                    | 121  | SFFNDAEE-----SKATIKDADSNCLKTSGI-----KSQD--CHS 154             | Db   | 258   | MTYEKLSSRLRYYYKTGILERVDRRLVYKFGNAHGWRENE 299   |                       |  |                       |  |
| Qy                    | 132 TIKD-YADSNCL-----KTSIGI-----KSQD---C 152   | RESULT                | 13   | Q99K12  | PRELIMINARY;   | PRT;  | 285 AA.  |                       |  |                       |  |
| Db                    | 138 SIANTWKEENLYDPSSYGTVDLDSKTCRAQISMSTSMLPVAESPDMKKEODHPAEC 197   | ID                    | Q99K12   | AC  | Q99K12;  | PRT;  | 285 AA.  |                       |  |                       |  |
| Qy                    | 153 HSRSRTSLOSSHLWEFVRDILLSPENCGILEWEDEREGIIFRVVKSEALAKMKGORKKNDR 212  | AC                    | Q99K12;  | DT  | 01-JUN-2001 (TREMBLER_17, Created)   | AC  | Q99K12;  | DT                    | 01-JUN-2001 (TREMBLER_17, Last sequence update)  | AC                    | Q99K12;  |
| Db                    | 198 HT-KKHHNPRTGTHWEIFRDILLSPDKNPGLIKEDRSEGVTFLKSEAVQLWGKKNNSS 256   | DB                    | 198  | HTKKHNPRTGTHWEIFRDILLSPDKNPGLIKEDRSEGVTFLKSEAVQLWGKKNNSS 257  | DR   | 01-DEC-2001 (TREMBLER_19, Last annotation update) | DB   | 198                   | HTKKHNPRTGTHWEIFRDILLSPDKNPGLIKEDRSEGVTFLKSEAVQLWGKKNNSS 257   | DR                    | 01-DEC-2001 (TREMBLER_19, Last annotation update)  |
| Qy                    | 213 RMTYEKLSSRLRYYYKTGILERVDRRLVYKFGNAHGWQDK 254   | DE                    | DE   | DE  | DE   | DE  | DE   | DE                    | DE   | DE                    | DE   |
| Db                    | 257 MTYEKLSSRLRYYYKTGILERVDRRLVYKFGNAHGWRENE 299   | OS                    | OS   | OS  | OS   | OS  | OS   | OS                    | OS   | OS                    | OS   |
| Qy                    | 257 MTYEKLSSRLRYYYKTGILERVDRRLVYKFGNAHGWRENE 299   | OC                    | OC   | OC  | OC   | OC  | OC   | OC                    | OC   | OC                    | OC   |
| Db                    | 257 MTYEKLSSRLRYYYKTGILERVDRRLVYKFGNAHGWRENE 299   | NCBI_TAXID=10090;     | NCBI_TAXID=10090;  | NCBI_TAXID=10090;   | NCBI_TAXID=10090;  | NCBI_TAXID=10090;                                 | NCBI_TAXID=10090;  | NCBI_TAXID=10090;     | NCBI_TAXID=10090;  | NCBI_TAXID=10090;     | NCBI_TAXID=10090;  |
| Qy                    | 257 MTYEKLSSRLRYYYKTGILERVDRRLVYKFGNAHGWRENE 299   | RN                    | RN   | RN  | RN   | RN  | RN   | RN                    | RN   | RN                    | RN   |
| DR                    | SEQUENCE FROM N.A.   | RP                    | SEQUENCE FROM N.A.   | RA  | SEQUENCE FROM N.A.   | RA  | SEQUENCE FROM N.A.   | RA                    | SEQUENCE FROM N.A.   | RA                    | SEQUENCE FROM N.A.   |
| DR                    | Strausberg R.;   | RL                    | Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.   | RL  | Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.   | RL  | Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.   | RL                    | Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.   | RL                    | Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.   |
| DR                    | EMBL; BC001520; AAH05520.1; -.   | DR                    | HSSP; Q00422; 1AWC   | DR  | InterPro; IPR000418; ETS   | DR  | InterPro; IPR002341; HSE-ETS   | DR                    | InterPro; IPR003118; SAM_PNT   | DR                    | InterPro; IPR00178; Ets_1  |
| DR                    | DR   | DR                    | DR   | DR  | DR   | DR  | DR   | DR                    | DR   | DR                    | DR   |
| DR                    | PRINTS; PRO0454; ETSDOMAIN.  | DR                    | SMART; SM00413; ETS; 1.  | DR  | PROSITE; PS50061; ETSDOMAIN_3; 1.  | DR  | PROSITE; PS50061; ETSDOMAIN_3; 1.  | DR                    | PROSITE; PS50061; ETSDOMAIN_3; 1.  | DR                    | PROSITE; PS50061; ETSDOMAIN_3; 1.  |
| DR                    | SMART; SM00251; SAM_PNT; 1.  | DR                    | SMART; SM00251; SAM_PNT; 1.  | DR  | SEQUENCE FROM N.A.   | DR  | SEQUENCE FROM N.A.   | DR                    | SEQUENCE FROM N.A.   | DR                    | SEQUENCE FROM N.A.   |
| DR                    | RC   | RC                    | RC   | RC  | RC   | RC  | RC   | RC                    | RC   | RC                    | RC   |
| DR                    | MEDLINE#36262938; PubMed#9600089;  | RA                    | RA   | RA  | RA   | RA  | RA   | RA                    | RA   | RA                    | RA   |
| DR                    | Bochet M.A., Kleinbaum L.A., Sun L.Y., Burton F.H./  | AC                    | AC   | AC  | AC   | AC  | AC   | AC                    | AC   | AC                    | AC   |
| RT                    | "Molecular cloning and expression of Ehf, a new member of the ets transcription factor/oncoprotein gene family." | DT                    | 01-07-1998 (TREMBLER_07, Created)  | DT  | 01-AUG-1998 (TREMBLER_07, Last sequence update)  | DT  | 01-DEC-2001 (TREMBLER_19, Last annotation update)  | DT                    | 01-DEC-2001 (TREMBLER_19, Last annotation update)  | DT                    | 01-DEC-2001 (TREMBLER_19, Last annotation update)  |
| DR                    | Biophys. Res. Commun. 246:176-181(1998).   | DR                    | EHFs.  | DR  | EHFs.  | DR  | EHFs.  | DR                    | EHFs.  | DR                    | EHFs.  |
| DR                    | EMBL; AF035527; AAC40119.1; -.   | DR                    | Mus musculus (Mouse),  | DR  | Mus musculus (Mouse),  | DR  | Mus musculus (Mouse),  | DR                    | Mus musculus (Mouse),  | DR                    | Mus musculus (Mouse),  |
| DR                    | MGI; MGI-1270840; Ehf.   | DR                    | Metaryota; Chordata; Craniata; Vertebrata; Euteleostomi;   | DR  | Metaryota; Chordata; Craniata; Vertebrata; Euteleostomi;   | DR  | Metaryota; Chordata; Craniata; Vertebrata; Euteleostomi;   | DR                    | Metaryota; Chordata; Craniata; Vertebrata; Euteleostomi;   | DR                    | Metaryota; Chordata; Craniata; Vertebrata; Euteleostomi;   |
| DR                    | InterPro; IPR000418; Ets.  | DR                    | Mammalia; Eutheria; Rodentia; Sciurognathii; Muridae; Murinae; Mus.  | DR  | Mammalia; Eutheria; Rodentia; Sciurognathii; Muridae; Murinae; Mus.  | DR  | Mammalia; Eutheria; Rodentia; Sciurognathii; Muridae; Murinae; Mus.  | DR                    | Mammalia; Eutheria; Rodentia; Sciurognathii; Muridae; Murinae; Mus.  | DR                    | Mammalia; Eutheria; Rodentia; Sciurognathii; Muridae; Murinae; Mus.  |
| DR                    | InterPro; IPR002341; HSE-ETS.  | DR                    | [1]  | DR  | [1]  | DR  | [1]  | DR                    | [1]  | DR                    | [1]  |
| DR                    | InterPro; IPR003118; SAM_PNT.  | DR                    | SEQUENCE FROM N.A.   | DR  | SEQUENCE FROM N.A.   | DR  | SEQUENCE FROM N.A.   | DR                    | SEQUENCE FROM N.A.   | DR                    | SEQUENCE FROM N.A.   |
| DR                    | Pfam; PF00178; Ets_1.  | DR                    | TMEDLINE#36262938; PubMed#9600089;   | DR  | TMEDLINE#36262938; PubMed#9600089;   | DR  | TMEDLINE#36262938; PubMed#9600089;   | DR                    | TMEDLINE#36262938; PubMed#9600089;   | DR                    | TMEDLINE#36262938; PubMed#9600089;   |
| DR                    | PRINTS; PRO0454; ETSDOMAIN.  | DR                    | RT   | RT  | RT   | RT  | RT   | RT                    | RT   | RT                    | RT   |
| DR                    | SMART; SM00413; ETS; 1.  | DR                    | "Molecular cloning and expression of Ehf, a new member of the ets transcription factor/oncoprotein gene family." | DR  | "Molecular cloning and expression of Ehf, a new member of the ets transcription factor/oncoprotein gene family." | DR  | "Molecular cloning and expression of Ehf, a new member of the ets transcription factor/oncoprotein gene family." | DR                    | "Molecular cloning and expression of Ehf, a new member of the ets transcription factor/oncoprotein gene family." | DR                    | "Molecular cloning and expression of Ehf, a new member of the ets transcription factor/oncoprotein gene family." |
| DR                    | SMART; SM00251; SAM_PNT; 1.  | DR                    | RT   | RT  | RT   | RT  | RT   | RT                    | RT   | RT                    | RT   |
| DR                    | PROSITE; PS50061; ETSDOMAIN_3; 1.  | DR                    | RT   | RT  | RT   | RT  | RT   | RT                    | RT   | RT                    | RT   |
| DR                    | SEQUENCE 300 AA; 34903 MN;   | DR                    | RT   | RT  | RT   | RT  | RT   | RT                    | RT   | RT                    | RT   |
| Qy                    | 40.3%; Score 568; DB 11; Length 300;   | Qy                    | 36.5%; Score 514.5; DB 11; Length 285;   | Qy  | 36.5%; Score 514.5; DB 11; Length 285;   | Qy  | 36.5%; Score 514.5; DB 11; Length 285;   | Qy                    | 36.5%; Score 514.5; DB 11; Length 285;   | Qy                    | 36.5%; Score 514.5; DB 11; Length 285;   |
| Best Local Similarity | 42.6%; Pred. No. 9.9e-47;  | Best Local Similarity | 39.7%; Pred. No. 1.3e-41;  | Best Local Similarity   | 39.7%; Pred. No. 1.3e-41;  | Best Local Similarity                             | 39.7%; Pred. No. 1.3e-41;  | Best Local Similarity | 39.7%; Pred. No. 1.3e-41;  | Best Local Similarity | 39.7%; Pred. No. 1.3e-41;  |

|                       |  |                                 |  |         |   |                       |   |                                |   |    |   |    |   |
|-----------------------|--|---------------------------------|--|---------|---|-----------------------|---|--------------------------------|---|----|---|----|---|
| Qy                    | 214 MTYEKLRSRALRYYYTGILERVD-RRLVYKFGKNAHGQWEDK   | 254                             | RESULT   | 14      | PRELIMINARY;  | PRT;                  | 371 AA.   | 15                             |   |    |   |    |   |
| Db                    | 243 MTYEKLRSRALRYYYREILERVDGRRVYKFGKNAHGQWENE  | 284                             | ID   | 035275  | PRELIMINARY;  | PRT;                  | 371 AA.   |                                |   |    |   |    |   |
|                       | ID 035275;   |                                 | AC   | 035275; |   |                       |   |                                |   |    |   |    |   |
|                       | DT 01-JAN-1998 (TRIMBLrel. 05; Created)  |                                 | DT 01-MAY-1997 (TRIMBLrel. 03; Last sequence update)   |         |   |                       |   |                                |   |    |   |    |   |
|                       | DT 01-JAN-1998 (TRIMBLrel. 05; Last sequence update)   |                                 | DT 01-MAY-1997 (TRIMBLrel. 03; Last annotation update)   |         |   |                       |   |                                |   |    |   |    |   |
|                       | DT 01-DEC-2001 (TRIMBLrel. 19; Last annotation update)   |                                 | DE ETS TRANSCRIPTION FACTOR.   |         |   |                       |   |                                |   |    |   |    |   |
|                       | GN ELF3 OR ERF3.   |                                 | GN ETS TRANSCRIPTION FACTOR.   |         |   |                       |   |                                |   |    |   |    |   |
| OS                    | Mus musculus (Mouse);  |                                 | OS Homo sapiens (Human)  |         |   |                       |   |                                |   |    |   |    |   |
| OC                    | Mammalia; Butheria; Rodentia; Sciurognathia; Muridae; Murinae; Mus.  |                                 | OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. |         |   |                       |   |                                |   |    |   |    |   |
| OX                    | NCBI_TaxID=9606;   |                                 | OX NCBI_TaxID=9606;  |         |   |                       |   |                                |   |    |   |    |   |
| RN                    | [1]  |                                 | RN [1]   |         |   |                       |   |                                |   |    |   |    |   |
| RP                    | SEQUENCE FROM N.A.   |                                 | RP SEQUENCE FROM N.A.  |         |   |                       |   |                                |   |    |   |    |   |
| RN                    | TISSUE="LUNG";   |                                 | RP TISSUE=LIVER, AND PANCREATIC CARCINOMA;   |         |   |                       |   |                                |   |    |   |    |   |
| RX                    | MEDLINE="9055619; PubMed=9395241;  |                                 | RX MEDLINE=97378019; PubMed=234700;  |         |   |                       |   |                                |   |    |   |    |   |
| RA                    | Tymms M.J., Ng A.Y., Thomas R.S., Schutte B.C., Zhou J., Eyre H.J.,  |                                 | RA Oettgen P., Alain R.M., Barcinski M.A., Brown L., Akbarali Y.,  |         |   |                       |   |                                |   |    |   |    |   |
| RA                    | Sutherland G.R., Seth A., Rosenberg M., Papas T., Debonck C., Kola I.,   |                                 | RA Boltax J., Kunsch C., Munger K., Libermann T.A.;  |         |   |                       |   |                                |   |    |   |    |   |
| RT                    | "A novel epithelial-expressed Ets gene, ELF3: human and murine cDNA sequences, murine genomic organization, human mapping to 1q32.2 and expression in tissues and cancer." |                                 | RT Isolation and characterization of a novel epithelium-specific transcription factor, ESE-1, a member of the ets family."         |         |   |                       |   |                                |   |    |   |    |   |
| RT                    | OncoGene 15:2449-2452(1997).   |                                 | RT Mol. Cell. Biol. 17:419-443(1997)   |         |   |                       |   |                                |   |    |   |    |   |
| DR                    | EMBL: AF06294; AAB6585.1; -.   |                                 | DR InterPro: IPR000637; AT_hook.   |         |   |                       |   |                                |   |    |   |    |   |
| DR                    | HSSP: P28324; IBC8.  |                                 | DR InterPro: IPR000418; Ets.   |         |   |                       |   |                                |   |    |   |    |   |
| DR                    | MGD: MGI:1101791; Eif3.  |                                 | DR InterPro: IPR003118; SAM_PNT.   |         |   |                       |   |                                |   |    |   |    |   |
| DR                    | InterPro: IPR000637; AT_hook.  |                                 | DR Pfam: PF00178; AT_hook; 1.  |         |   |                       |   |                                |   |    |   |    |   |
| DR                    | InterPro: IPR00418; Ets.   |                                 | DR Pfam: PF00178; Ets; 1.  |         |   |                       |   |                                |   |    |   |    |   |
| DR                    | InterPro: IPR002341; HSP_ETS.  |                                 | DR PRINTS: PRO0454; ETS_DOMAIN.  |         |   |                       |   |                                |   |    |   |    |   |
| DR                    | InterPro: IPR003118; SAM_PNT.  |                                 | DR SMART: SM00384; AT_hook; 1.   |         |   |                       |   |                                |   |    |   |    |   |
| DR                    | Pfam: PF00178; AT_hook; 1.   |                                 | DR SMART: SM00413; ETS; 1.   |         |   |                       |   |                                |   |    |   |    |   |
| DR                    | Pfam: PF00198; SAM_PNT; 1.   |                                 | DR SMART: SM00251; SAM_PNT; 1.   |         |   |                       |   |                                |   |    |   |    |   |
| DR                    | PRINTS: PRO0454; ETS_DOMAIN.   |                                 | DR PROSITE: PS50061; ETS_DOMAIN_3; 1.  |         |   |                       |   |                                |   |    |   |    |   |
| DR                    | SMART: SM00384; AT_hook; 1.  |                                 | DR SEQUENCE: 348 AA; 39357 MW; AE2A6D3633CA305E CRC64;   |         |   |                       |   |                                |   |    |   |    |   |
| DR                    | SMART: SM00413; ETS; 1.  |                                 |  |         |   |                       |   |                                |   |    |   |    |   |
| DR                    | SMART: SM00251; SAM_PNT; 1.  |                                 |  |         |   |                       |   |                                |   |    |   |    |   |
| DR                    | PROSITE: PS50061; ETS_DOMAIN_3; 1.   |                                 |  |         |   |                       |   |                                |   |    |   |    |   |
| SQ                    | SEQUENCE: 371 AA; 42060 MW;  | 042BDACC05839EE6 CRC64;         |  |         |   |                       |   |                                |   |    |   |    |   |
| Query Match           | 30.6%  | Score 430.5; DB 11; Length 371; | Query Match  | 30.3%   | Score 427.5; DB 4; Length 348;                                      | Query Match           | 30.3%   | Score 427.5; DB 4; Length 348; |   |    |   |    |   |
| Best Local Similarity | 30.7%  | Pred. No. 2.4e-33;              | Best Local Similarity  | 31.0%   | Pred. No. 4.3e-33;  | Best Local Similarity | 31.0%   | Pred. No. 4.3e-33;             |   |    |   |    |   |
| Matches               | 95;  | Mismatches 47; Gaps 68;         | Matches  | 89;     | Mismatches 49;  | Matches               | 89;   | Mismatches 49;                 |   |    |   |    |   |
| Qy                    | 46 WTSVHPEYWTKRHYNEWLQFCDOYKVLDTNCISPCNFNTISQLQCSMTQEVEVAGLCG 105  | Db                              | 46 WTSVHPEYWTKRHYNEWLQFCDOYKVLDTNCISPCNFNTISQLQCSMTQEVEVAGLCG 105  | Db      | 46 WTSVHPEYWTKRHYNEWLQFCDOYKVLDTNCISPCNFNTISQLQCSMTQEVEVAGLCG 105   | Qy                    | 46 WTSVHPEYWTKRHYNEWLQFCDOYKVLDTNCISPCNFNTISQLQCSMTQEVEVAGLCG 105   | Db                             | 46 WTSVHPEYWTKRHYNEWLQFCDOYKVLDTNCISPCNFNTISQLQCSMTQEVEVAGLCG 105 |    |   |    |   |
| Db                    | 58 WTSEPOFWSKTQVLEWISTQVKRYDASSIDEFSRCDMDGATLCSCALEBLRLVFGPLG 117  | Qy                              | 58 WTSEPOFWSKTQVLEWISTQVKRYDASSIDEFSRCDMDGATLCSCALEBLRLVFGPLG 117  | Db      | 59 WGEQPFQWSRSTQVLDWISYKEVKNYKDASIDEFSRCDMDGATLCSCALEBLRLVFGPLG 118 | Db                    | 59 WGEQPFQWSRSTQVLDWISYKEVKNYKDASIDEFSRCDMDGATLCSCALEBLRLVFGPLG 118 | Qy                             | 58 WTSEPOFWSKTQVLEWISTQVKRYDASSIDEFSRCDMDGATLCSCALEBLRLVFGPLG 117 | Db | 59 WGEQPFQWSRSTQVLDWISYKEVKNYKDASIDEFSRCDMDGATLCSCALEBLRLVFGPLG 118 |    |   |
| Qy                    | 106 EYLY-----FILQNRTQGYSF-----FNDAEESK 130   | Db                              | 106 EYLY-----FILQNRTQGYSF-----FNDAEESK 130   | Qy      | 106 EYLY-----FILQNRTQGYSF-----FNDAEESK 130                          | Db                    | 106 EYLY-----FILQNRTQGYSF-----FNDAEESK 130                          | Qy                             | 106 EYLY-----FILQNRTQGYSF-----FNDAEESK 130                        | Db | 106 EYLY-----FILQNRTQGYSF-----FNDAEESK 130                          |    |   |
| Db                    | 118 DQLHAQRDLTSNSSDDELNSWIELLEKDGNFSQESLGDSGPFDQGSPPAQELLDGQAS 177   | Qy                              | 118 DQLHAQRDLTSNSSDDELNSWIELLEKDGNFSQESLGDSGPFDQGSPPAQELLDGQAS 177   | Db      | 119 DOLHAQRDLTSSSDELSWIELLEKDGMFAQEALDGPFDQGSPPAQELLDGQAS 178       | Qy                    | 118 DOLHAQRDLTSSSDELSWIELLEKDGMFAQEALDGPFDQGSPPAQELLDGQAS 177       | Db                             | 119 DOLHAQRDLTSSSDELSWIELLEKDGMFAQEALDGPFDQGSPPAQELLDGQAS 178     | Qy | 118 DQLHAQRDLTSNSSDDELNSWIELLEKDGNFSQESLGDSGPFDQGSPPAQELLDGQAS 177  | Db | 119 DOLHAQRDLTSSSDELSWIELLEKDGMFAQEALDGPFDQGSPPAQELLDGQAS 177     |
| Qy                    | 131 -----ATIK-----DADSNCNLKTSGIKSQ-- 150   | Db                              | 131 -----ATIK-----DADSNCNLKTSGIKSQ-- 150   | Qy      | 131 -----ATIK-----DADSNCNLKTSGIKSQ-- 150                            | Db                    | 131 -----ATIK-----DADSNCNLKTSGIKSQ-- 150                            | Qy                             | 131 -----ATIK-----DADSNCNLKTSGIKSQ-- 150                          | Db | 131 -----ATIK-----DADSNCNLKTSGIKSQ-- 150                            |    |   |
| Db                    | 178 PYYCSTYGPAPSPGSSDVSTARTPQSSHASDGGSDYDLDLPSKVPFRGPDYKK 237  | Qy                              | 178 PYYCSTYGPAPSPGSSDVSTARTPQSSHASDGGSDYDLDLPSKVPFRGPDYKK 237  | Db      | 178 PYYCSTYGPAPSPGSSDVSTARTPQSSHASDGGSDYDLDLPSKVPFRGPDYKK 237       | Qy                    | 178 PYYCSTYGPAPSPGSSDVSTARTPQSSHASDGGSDYDLDLPSKVPFRGPDYKK 237       | Db                             | 178 PYYCSTYGPAPSPGSSDVSTARTPQSSHASDGGSDYDLDLPSKVPFRGPDYKK 237     | Qy | 178 PYYCSTYGPAPSPGSSDVSTARTPQSSHASDGGSDYDLDLPSKVPFRGPDYKK 237       | Db | 178 PYYCSTYGPAPSPGSSDVSTARTPQSSHASDGGSDYDLDLPSKVPFRGPDYKK 237     |
| Qy                    | 151 -----DC-HSHSRSTSLOSSHILWEPYRDLILSPEENCGILEWEED 187   | Db                              | 151 -----DC-HSHSRSTSLOSSHILWEPYRDLILSPEENCGILEWEED 187   | Qy      | 151 -----DC-HSHSRSTSLOSSHILWEPYRDLILSPEENCGILEWEED 187              | Db                    | 151 -----DC-HSHSRSTSLOSSHILWEPYRDLILSPEENCGILEWEED 187              | Qy                             | 151 -----DC-HSHSRSTSLOSSHILWEPYRDLILSPEENCGILEWEED 187            | Db | 151 -----DC-HSHSRSTSLOSSHILWEPYRDLILSPEENCGILEWEED 187              |    |   |
| Db                    | 238 GEPKIGKRKGRRPKLRSKEYWDCLGSKSKHAPRGLWTFIRDLIHPNELNEGJMKWEN 297  | Qy                              | 188 REQKIFRVKVSSEALKMKGQKKNNDRMTYKLSRALRYYKGTGILERVD-RRLVYKFGK 246   | Db      | 238 GEPKIGKRKGRRPKLRSKEYWDCLGSKSKHAPRGLWTFIRDLIHPNELNEGJMKWEN 297   | Qy                    | 188 REQKIFRVKVSSEALKMKGQKKNNDRMTYKLSRALRYYKGTGILERVD-RRLVYKFGK 246  | Db                             | 238 GEPKIGKRKGRRPKLRSKEYWDCLGSKSKHAPRGLWTFIRDLIHPNELNEGJMKWEN 297 | Qy | 188 REQKIFRVKVSSEALKMKGQKKNNDRMTYKLSRALRYYKGTGILERVD-RRLVYKFGK 246  | Db | 238 GEPKIGKRKGRRPKLRSKEYWDCLGSKSKHAPRGLWTFIRDLIHPNELNEGJMKWEN 297 |
| Qy                    | 298 RHEGFKFLRSEAVQLGQKKSMMTYKLSRAMYYKREILLERVGRLVYKFGK 357   | Db                              | 298 RHEGFKFLRSEAVQLGQKKSMMTYKLSRAMYYKREILLERVGRLVYKFGK 357   | Qy      | 298 RHEGFKFLRSEAVQLGQKKSMMTYKLSRAMYYKREILLERVGRLVYKFGK 357          | Db                    | 298 RHEGFKFLRSEAVQLGQKKSMMTYKLSRAMYYKREILLERVGRLVYKFGK 357          | Qy                             | 298 RHEGFKFLRSEAVQLGQKKSMMTYKLSRAMYYKREILLERVGRLVYKFGK 357        | Db | 298 RHEGFKFLRSEAVQLGQKKSMMTYKLSRAMYYKREILLERVGRLVYKFGK 357          |    |   |

Search completed: August 13, 2002, 21:31:15  
 Job time: 565 sec

